

Title

Effect of temperature, sex, sire-specific genetics and their interactions on the gonadal epigenetic patterns of the European sea bass (*Dicentrarchus labrax*)

Speaker

SANCHEZ-BAIZAN Nuria, Institute Marine Sciences Barcelona – SPAIN (nsbaizan@icm.csic.es)

Authors list

Sánchez-Baizán N., Anastasiadi D., Vandeputte M., Allal F., Piferrer F.

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Abstract

The European sea bass still presents important challenges to production under captivity, such as sexual growth dimorphism. In general, males grow slower than females and reach weights about 30% less at the harvest size. Farmed fish show male bias with percentages of up to 90%. The study of sex development contributes to the improvement of farming methodologies. The European sea bass has a polygenic sex determining system with temperature effects during the larval stage, which causes masculinization in a proportion of the stock. In a previous study, we created four families and exposed their larvae to low (LT) and high temperatures (HT). The DNA methylation profile of seven genes related to sexual development was examined in juvenile gonads (F1, one year). The genes most affected by both genetics and environment were *cyp19a1a* and *dmrt1*, with opposite responses to sex and temperature. Based on methylation levels of most informative CpGs and a machine-learning procedure, it was possible to develop a system for sex prediction. In the following study, we created eight families by crossing an external female with eight males among the F1: two LT, three HT and three HT neomales (NM), which were identified by genotype analysis. Based on phenotypic and genotypic data of the F2 offspring we selected individuals representative of each group according to their sex, temperature during development and sire type. Next, we are going to analyze the DNA methylation profiles of grandparents' gametes (F0, n=2), sires and dam gametes (F1, n=9) and offspring juvenile gonad (F2, n=119) by Reduced Representation Bisulfite sequencing. With this approach, we will obtain information on the epigenetic patterns at the genome-wide level, which will enable us to investigate grandparent, parent-to-offspring relationships, the conserved epigenetic effect of temperature regardless of the family, and the potential additive effect of temperature among the individuals exposed in multiple generations.